

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

Claim 1 (Cancelled)

2. (Original) An isolated negative-sense single stranded RNA virus (MPV) belonging to the sub-family *Pneumovirinae* of the family *Paramyxoviridae* and identifiable as phylogenetically corresponding to the genus *Metapneumovirus* by determining a nucleic acid sequence of said virus and testing it in phylogenetic tree analyses wherein maximum likelihood trees are generated using 100 bootstraps and 3 jumbles and finding it to be more closely phylogenetically corresponding to a virus isolate deposited as **I-2614** with CNCM, Paris than it is corresponding to a virus isolate of avian pneumovirus (APV) also known as turkey rhinotracheitis virus (TRTV), the aetiological agent of avian rhinotracheitis.

Claims 3 to 58 (Cancelled)

59. (Currently amended) A method for detecting a human metapneumovirus in a sample. ~~The method of claim 48, 49, 50 or 51,~~ wherein the method ~~further~~ comprises contacting the sample with a nucleic acid encoding an amino acid sequence that is:

- (a) an amino acid sequence that is greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1 or 99-1 as shown in Figure 20;
- (b) an amino acid sequence that is greater than 68% identical to the amino acid sequence of the P protein of MPV isolate 00-1 or 99-1 as shown in Figure 21;
- (c) an amino acid sequence that is greater than 87% identical to the amino acid sequence of the M protein of MPV isolate 00-1 or 99-1 as shown in Figure 22;
- (d) an amino acid sequence that is greater than 81% identical to the amino acid sequence of the F protein of MPV isolate 00-1 or 99-1 as shown in Figure 23;
- (e) an amino acid sequence that is greater than 84% identical to the amino acid sequence of the M2-1 protein of MPV isolate 00-1 or 99-1 as shown in Figure 24;

- (f) an amino acid sequence that is greater than 56% identical to the amino acid sequence of the M2-2 protein of MPV isolate 00-1 or 99-1 as shown in Figure 25;
- (g) an amino acid sequence that is greater than 90% identical to the amino acid sequence of the L protein of MPV isolate 00-1 or 99-1 as shown in Figure 28;
- (h) an amino acid sequence that is greater than 29% identical to the amino acid sequence of the SH protein of MPV isolate 00-1 or 99-1 as shown in Figure 26; or
- (i) an amino acid sequence that is greater than 29% identical to the amino acid sequence of the G protein of MPV isolate 00-1 or 99-1 as shown in Figure 27.

60. (Currently amended) A method for detecting a human metapneumovirus in a sample, The method of claim 48, 49, 50 or 51, wherein the method ~~further~~ comprises contacting the sample with an antibody that specifically binds to a protein that is:

- (a) greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1 or 99-1 as shown in Figure 20;
- (b) greater than 68% identical to the amino acid sequence of the P protein of MPV isolate 00-1 or 99-1 as shown in Figure 21;
- (c) greater than 87% identical to the amino acid sequence of the M protein of MPV isolate 00-1 or 99-1 as shown in Figure 22;
- (d) greater than 81 % identical to the amino acid sequence of the F protein of MPV isolate 00-1 or 99-1 as shown in Figure 23;
- (e) greater than 84% identical to the amino acid sequence of the M2-1 protein of MPV isolate 00-1 or 99-1 as shown in Figure 24;
- (f) greater than 56% identical to the amino acid sequence of the M2-2 protein of MPV isolate 00-1 or 99-1 as shown in Figure 25;
- (g) greater than 90% identical to the amino acid sequence of the L protein of MPV isolate 00-1 or 99-1 as shown in Figure 28;
- (h) greater than 29% identical to the amino acid sequence of the SH protein of MPV isolate 00-1 or 99-1 as shown in Figure 26; or
- (i) greater than 29% identical to the amino acid sequence of the G protein of MPV isolate 00-1 or 99-1 as shown in Figure 27.

61. (Currently amended) A method for detecting a human metapneumovirus in a sample, The method of claim 48, 49, 50 or 51, wherein the method ~~further~~ comprises

contacting the sample with a first group of one or more nucleic acids that hybridize under stringent conditions to a second group of one or more nucleic acids, that encodes a protein, or fragment thereof, comprising,

- (a) a sequence that is greater than 88% identical to the amino acid sequence of the N protein of MPV isolate 00-1 and 99-1 as shown in figure 20;
 - (b) a sequence that is greater than 68% identical to the amino acid sequence of the P protein of MPV isolate 00-1 and 99-1 as shown in figure 21;
 - (c) a sequence that is greater than 87% identical to the amino acid sequence of the M protein of MPV isolate 00-1 and 99-1 as shown in figure 22;
 - (d) a sequence that is greater than 81% identical to the amino acid sequence of the F protein of MPV isolate 00-1 and 99-1 as shown in figure 23;
 - (e) a sequence that is greater than 84% identical to the amino acid sequence of the M2-1 protein of MPV isolate 00-1 and 99-1 as shown in figure 24;
 - (f) a sequence that is greater than 56% identical to the amino acid sequence of the M2-2 protein of MPV isolate 00-1 and 99-1 as shown in figure 25;
 - (g) a sequence that is greater than 90% identical to the amino acid sequence of the L protein of MPV isolate 00-1 and 99-1 as shown in figure 28;
 - (h) a sequence that is greater than 29% identical to the amino acid sequence of the SH protein of MPV isolate 00-1 and 99-1 as shown in figure 26; or
 - (i) a sequence that is greater than 29% identical to the amino acid sequence of the G protein of MPV isolate 00-1 and 99-1 as shown in figure 27,
- wherein sequence identity is determined over the entire length of the protein.

62. (Currently amended) A method for detecting a human metapneumovirus in a sample. The method of claim 48, 49, 50 or 51, wherein the method further comprises contacting the sample with one or more nucleic acids that hybridize under stringent conditions to the genome or antigenome of the virus isolate deposited as I-2614 with CNCM, Paris.

63. (New) The method of claim 59, wherein the amino acid is:
- (i) SEQ ID No.: 64 or 98;
 - (ii) SEQ ID No.: 21 or 94;
 - (iii) SEQ ID No.: 99 or 100;
 - (iv) SEQ ID No.: 47 or 95;

- (v) SEQ ID No.: 55 or 96;
- (vi) SEQ ID No.: 14 or 93;
- (vii) SEQ ID No.: 1 or 91;
- (viii) SEQ ID No.: 8 or 92; or
- (ix) SEQ ID No.: 63 or 97.

64. (New) A method for detecting a human metapneumovirus in a sample, wherein the method comprises contacting the sample with a primer selected from the group consisting of SEQ ID No.: 113-120.

65. (New) A method for detecting a human metapneumovirus in a sample, wherein the method comprises contacting the sample with a probe having the nucleic acid sequence of SEQ ID No.: 121, 122 or 123.

66. (New) The method of claim 60, wherein the protein consists of an amino acid sequence of:

- (i) SEQ ID No.: 64 or 98;
- (ii) SEQ ID No.: 21 or 94;
- (iii) SEQ ID No.: 99 or 100;
- (iv) SEQ ID No.: 47 or 95;
- (v) SEQ ID No.: 55 or 96;
- (vi) SEQ ID No.: 14 or 93;
- (vii) SEQ ID No.: 1 or 91;
- (viii) SEQ ID No.: 8 or 92; or
- (ix) SEQ ID No.: 63 or 97.

67. (New) The method of claim 66, wherein the method further comprises an immune fluorescence assay.

68. (New) A method for detecting an antibody against human metapneumovirus in a sample, wherein the method comprises contacting the sample with a protein comprising the amino acid sequence of:

- (i) SEQ ID No.: 64 or 98;
- (ii) SEQ ID No.: 21 or 94;

- (iii) SEQ ID No.: 99 or 100;
- (iv) SEQ ID No.: 47 or 95;
- (v) SEQ ID No.: 55 or 96;
- (vi) SEQ ID No.: 14 or 93;
- (vii) SEQ ID No.: 1 or 91;
- (viii) SEQ ID No.: 8 or 92; or
- (ix) SEQ ID No.: 63 or 97.